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RAW SEQUENCE LISTING

DATE: 10/08/2002

PATENT APPLICATION: US/09/841,720D

TIME: 13:42:58

Input Set : A:\INDA002USD1.APP

Output Set: N:\CRF4\10082002\I841720D.raw

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3 <110> APPLICANT: YU, LEI
5 <120> TITLE OF INVENTION: MU OPIOID RECEPTOR: COMPOSITIONS AND METHODS
7 <130> FILE REFERENCE: INDA:002USD1
9 <140> CURRENT APPLICATION NUMBER: 09/841,720D
10 <141> CURRENT FILING DATE: 2001-04-24
12 <150> PRIOR APPLICATION NUMBER: 08/120,601
13 <151> PRIOR FILING DATE: 1993-09-13
15 <160> NUMBER OF SEQ ID NOS: 9
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1618
21 <212> TYPE: DNA
22 <213> ORGANISM: RAT
24 <220> FEATURE:
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26 <222> LOCATION: (214)..(1407)
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33 gctgtgagag gaagaggctg gggcgcgtgg aaccgaaaa gtctgagtgc tctcagttac 180
35 agcctaccta gtcgcagca ggccttcagc acc atg gac agc acc ggc cca 234
36                               Met Asp Ser Ser Thr Gly Pro
37                               1               5
39 ggg aac acc agc gac tgc tca gac ccc tta gct cag gca agt tgc tcc 282
40 Gly Asn Thr Ser Asp Cys Ser Asp Pro Leu Ala Gln Ala Ser Cys Ser
41       10               15               20
43 cca gca cct ggc tcc tgg ctc aac ttg tcc cac gtt gat ggc aac cag 330
44 Pro Ala Pro Gly Ser Trp Leu Asn Leu Ser His Val Asp Gly Asn Gln
45       25               30               35
47 tcc gat cca tgc ggt ctg aac cgc acc ggg ctt ggc ggg aac gac agc 378
48 Ser Asp Pro Cys Gly Leu Asn Arg Thr Gly Leu Gly Gly Asn Asp Ser
49 40               45               50               55
51 ctg tgc cct cag acc ggc agc cct tcc atg gtc aca gcc att acc atc 426
52 Leu Cys Pro Gln Thr Gly Ser Pro Ser Met Val Thr Ala Ile Thr Ile
53       60               65               70
55 atg gcc ctc tac tct atc gtg tgt gta gtg ggc ctc ttc gga aac ttc 474
56 Met Ala Leu Tyr Ser Ile Val Cys Val Val Gly Leu Phe Gly Asn Phe
57       75               80               85
59 ctg gtc atg tat gtg att gta aga tac acc aaa atg aag act gcc acc 522
60 Leu Val Met Tyr Val Ile Val Arg Tyr Thr Lys Met Lys Thr Ala Thr
61       90               95               100
63 aac atc tac att ttc aac ctt gct ctg gca gac gcc tta gcg acc agt 570
64 Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu Ala Thr Ser

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67 aca ctg ccc ttt cag agt gtc aac tac ctg atg gga aca tgg ccc ttc 618
68 Thr Leu Pro Phe Gln Ser Val Asn Tyr Leu Met Gly Thr Trp Pro Phe
69 120      125      130      135
71 gga acc atc ctc tgc aag atc gtg atc tca ata gat tac tac aac atg 666
72 Gly Thr Ile Leu Cys Lys Ile Val Ile Ser Ile Asp Tyr Tyr Asn Met
73      140      145      150
75 ttc acc agc ata ttc acc ctc tgc acc atg agc gtg gac cgc tac att 714
76 Phe Thr Ser Ile Phe Thr Leu Cys Thr Met Ser Val Asp Arg Tyr Ile
77      155      160      165
79 gct gtc tgc cac cca gtc aaa gcc ctg gat ttc cgt acc ccc cga aat 762
80 Ala Val Cys His Pro Val Lys Ala Leu Asp Phe Arg Thr Pro Arg Asn
81      170      175      180
83 gcc aaa atc gtc aac gtc tgc aac tgg atc ctc tct tct gcc atc ggt 810
84 Ala Lys Ile Val Asn Val Cys Asn Trp Ile Leu Ser Ser Ala Ile Gly
85      185      190      195
87 ctg cct gta atg ttc atg gca acc aca aaa tac agg cag ggg tcc ata 858
88 Leu Pro Val Met Phe Met Ala Thr Thr Lys Tyr Arg Gln Gly Ser Ile
89 200      205      210      215
91 gat tgc acc ctc acg ttc tcc cac cca acc tgg tac tgg gag aac ctg 906
92 Asp Cys Thr Leu Thr Phe Ser His Pro Thr Trp Tyr Trp Glu Asn Leu
93      220      225      230
95 ctc aaa atc tgt gtc ttt atc ttc gct ttc atc atg ccg atc ctc atc 954
96 Leu Lys Ile Cys Val Phe Ile Phe Ala Phe Ile Met Pro Ile Leu Ile
97      235      240      245
99 atc act gtg tgt tac ggc ctg atg atc tta cga ctc aag agc gtt cgc 1002
100 Ile Thr Val Cys Tyr Gly Leu Met Ile Leu Arg Leu Lys Ser Val Arg
101      250      255      260
103 atg cta tcg ggc tcc aaa gaa aag gac agg aat ctg cgc agg atc acc 1050
104 Met Leu Ser Gly Ser Lys Glu Lys Asp Arg Asn Leu Arg Arg Ile Thr
105      265      270      275
107 cgg atg gtg ctg gtg gtc gtg gct gta ttt atc gtc tgc tgg acc ccc 1098
108 Arg Met Val Leu Val Val Val Ala Val Phe Ile Val Cys Trp Thr Pro
109 280      285      290      295
111 atc cac atc tac gtc atc atc aaa gcg ctg atc acg att cca gaa acc 1146
112 Ile His Ile Tyr Val Ile Ile Lys Ala Leu Ile Thr Ile Pro Glu Thr
113      300      305      310
115 aca ttt cag acc gtt tcc tgg cac ttc tgc att gct ttg ggt tac acg 1194
116 Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile Ala Leu Gly Tyr Thr
117      315      320      325
119 aac agc tgc ctg aat cca gtt ctt tac gcc ttc ctg gat gaa aac ttc 1242
120 Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe
121      330      335      340
123 aag cga tgc ttc aga gag ttc tgc atc cca acc tcg tcc acg atc gaa 1290
124 Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Thr Ile Glu
125      345      350      355
127 cag caa aac tcc act cga gtc cgt cag aac act agg gaa cat ccc tcc 1338
128 Gln Gln Asn Ser Thr Arg Val Arg Gln Asn Thr Arg Glu His Pro Ser
129 360      365      370      375

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131 acg gct aat aca gtg gat cga act aac cac cag cta gaa aat ctg gag 1386
132 Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Leu Glu Asn Leu Glu
133 380 385 390
135 gca gaa act gct cca ttg ccc taactgggtc tcacaccatc cagaccctcg 1437
136 Ala Glu Thr Ala Pro Leu Pro
137 395
139 ctaagcttag aggccgccat ctacgtggaa tcaggttgct gtcaggggtgt gtgggagggt 1497
141 ctggtttcct gagaaacccat ctgatcctgc attcaaagtc attcctctct ggctacttca 1557
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160 Ser His Val Asp Gly Asn Gln Ser Asp Pro Cys Gly Leu Asn Arg Thr
161 35 40 45
163 Gly Leu Gly Gly Asn Asp Ser Leu Cys Pro Gln Thr Gly Ser Pro Ser
164 50 55 60
166 Met Val Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val Cys Val
167 65 70 75 80
169 Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val Arg Tyr
170 85 90 95
172 Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu
173 100 105 110
175 Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val Asn Tyr
176 115 120 125
178 Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile Val Ile
179 130 135 140
181 Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Cys Thr
182 145 150 155 160
184 Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu
185 165 170 175
187 Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Val Asn Val Cys Asn Trp
188 180 185 190
190 Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala Thr Thr
191 195 200 205
193 Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser His Pro
194 210 215 220
196 Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile Phe Ala
197 225 230 235 240
199 Phe Ile Met Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Ile
200 245 250 255
202 Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu Lys Asp
203 260 265 270

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205 Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val Ala Val
206      275      280      285
208 Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile Lys Ala
209      290      295      300
211 Leu Ile Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp His Phe
212 305      310      315      320
214 Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val Leu Tyr
215      325      330      335
217 Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe Cys Ile
218      340      345      350
220 Pro Thr Ser Ser Thr Ile Glu Gln Gln Asn Ser Thr Arg Val Arg Gln
221      355      360      365
223 Asn Thr Arg Glu His Pro Ser Thr Ala Asn Thr Val Asp Arg Thr Asn
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227 385      390      395
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245 gctgtgagag gaagaggctg gggcgcgctg aaccogaaaa gtctgagtgc tctcagttac 180
247 agcctaccta gtccgcagca ggccttcagc accatggaca gcagcaccgg cccagggaac 240
249 accagcgact gctcagaccc cttagctcag gcaagttgct cccagcacc tggctcctgg 300
251 ctcaacttgt cccacgttga tggcaaccag tccgatcc atg cgg tct gaa ccg cac 356
252      Met Arg Ser Glu Pro His
253      1      5
255 cgg gct tgg cgg gaa cga cag cct gtg ccc tca gac cgg cag ccc ttc 404
256 Arg Ala Trp Arg Glu Arg Gln Pro Val Pro Ser Asp Arg Gln Pro Phe
257      10      15      20
259 cat ggt cac agc cat tac cat cat ggc cct cta ctc tat cgt gtg tgt 452
260 His Gly His Ser His Tyr His His Gly Pro Leu Leu Tyr Arg Val Cys
261      25      30      35
263 agt ggg cct ctt cgg aaa ctt cct ggt cat gta tgt gat tgt aag ata 500
264 Ser Gly Pro Leu Arg Lys Leu Pro Gly His Val Cys Asp Cys Lys Ile
265      40      45      50
267 cac caa aat gaa gac tgc cac caa cat cta cat ttt caa cct tgc tct 548
268 His Gln Asn Glu Asp Cys His Gln His Leu His Phe Gln Pro Cys Ser
269 55      60      65      70
271 ggc aga cgc ctt agc gac cag tac act gcc ctt tca gag tgt caa cta 596
272 Gly Arg Arg Leu Ser Asp Gln Tyr Thr Ala Leu Ser Glu Cys Gln Leu
273      75      80      85
275 cct gat ggg aac atg gcc ctt cgg aac cat cct ctg caa gat cgt gat 644
276 Pro Asp Gly Asn Met Ala Leu Arg Asn His Pro Leu Gln Asp Arg Asp

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279 ctc aat aga tta cta caa cat gtt cac cag cat att cac cct ctg cac 692
280 Leu Asn Arg Leu Leu Gln His Val His Gln His Ile His Pro Leu His
281          105          110          115
283 cat gag cgt gga ccg cta cat tgc tgt ctg cca ccc agt caa agc cct 740
284 His Glu Arg Gly Pro Leu His Cys Cys Leu Pro Pro Ser Gln Ser Pro
285          120          125          130
287 gga ttt ccg tac ccc ccg aaa tgc caa aat cgt caa cgt ctg caa ctg 788
288 Gly Phe Pro Tyr Pro Pro Lys Cys Gln Asn Arg Gln Arg Leu Gln Leu
289          135          140          145          150
291 gat cct ctc ttc tgc cat cgg tct gcc tgt aat gtt cat ggc aac cac 836
292 Asp Pro Leu Phe Cys His Arg Ser Ala Cys Asn Val His Gly Asn His
293          155          160          165
295 aaa ata cag gca ggg gtc cat aga ttg cac cct cac gtt ctc cca ccc 884
296 Lys Ile Gln Ala Gly Val His Arg Leu His Pro His Val Leu Pro Pro
297          170          175          180
299 aac ctg gta ctg gga gaa cct gct caa aat ctg tgt ctt tat ctt cgc 932
300 Asn Leu Val Leu Gly Glu Pro Ala Gln Asn Leu Cys Leu Tyr Leu Arg
301          185          190          195
303 ttt cat cat gcc gat cct cat cat cac tgt gtg tta cgg cct gat gat 980
304 Phe His His Ala Asp Pro His His His Cys Val Leu Arg Pro Asp Asp
305          200          205          210
307 ctt acg act caa gag cgt tcg cat gct atc ggg ctc caa aga aaa gga 1028
308 Leu Thr Thr Gln Glu Arg Ser His Ala Ile Gly Leu Gln Arg Lys Gly
309          215          220          225          230
311 cag gaa tct gcg cag gat cac ccg gat ggt gct ggt ggt cgt ggc tgt 1076
312 Gln Glu Ser Ala Gln Asp His Pro Asp Gly Ala Gly Gly Arg Gly Cys
313          235          240          245
315 att tat cgt ctg ctg gac ccc cat cca cat cta cgt cat cat caa agc 1124
316 Ile Tyr Arg Leu Leu Asp Pro His Pro His Leu Arg His His Gln Ser
317          250          255          260
319 gct gat cac gat tcc aga aac cac att tca gac cgt ttc ctg gca ctt 1172
320 Ala Asp His Asp Ser Arg Asn His Ile Ser Asp Arg Phe Leu Ala Leu
321          265          270          275
323 ctg cat tgc ttt ggg tta cac gaa cag ctg cct gaa tcc agt tct tta 1220
324 Leu His Cys Phe Gly Leu His Glu Gln Leu Pro Glu Ser Ser Ser Leu
325          280          285          290
327 cgc ctt cct gga tgaaaacttc aagcgatgct tcagagagtt ctgcatccca 1272
328 Arg Leu Pro Gly
329 295
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337 gccatctacg tggaatcagg ttgctgtcag ggtgtgtggg aggctctggt ttcctgagaa 1512
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VERIFICATION SUMMARY

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